MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2022-04-23, 10:36 based on data in: `/home/khoidnyds/RNAseq_old/9.features`

General Statistics

Copy table | Configure Columns | Plot | Showing 6/6 rows and 2/2 columns.

Sample Name	% Assigned	M Assigned
SRR14689338_mixed	61.0%	7.4
SRR14689339_mixed	59.2%	8.2
SRR14689340_lymphoblastic	59.5%	8.2
SRR14689341_lymphoblastic	51.1%	7.5
SRR14689344_myeloid	58.0%	8.1
SRR14689345_myeloid	59.1%	8.2

featureCounts

Subread featureCounts is a highly efficient general-purpose read summarization program that counts mapped reads for genomic features such as genes, exons, promoter, gene bodies, genomic bins and chromosomal locations. *DOI: 10.1093/bioinformatics/btt656.*

Number of Reads | Percentages